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hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
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HMM file:                /data/isb2k/blastdb/Pfam72/Pfam72
Sequence file:           /u/legal/jennyb/pf619.seq
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Query:  4325626CD1


Scores for sequence family classification (score includes all domains):
Model      Description                                   Score    E-value  N
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TBC        TBC domain                                    33.3     9.9e-10  1


Parsed for domains:
Model      Domain   seq-f  seq-t     hmm-f  hmm-t      score  E-value
--------   ------   -----  -----     -----  -----      -----  -------
TBC         1/1      98    315  ..     1    341  []     33.3  9.9e-10


Alignments of top-scoring domains:
TBC: domain 1 of 1, from 98 to 315: score 33.3, E = 9.9e-10
                   *->vrqgvpsslRgkVWklllgaqelnnclltdnfkgldlfglvpvllla
                      +g p + Rg  W +ll++ e+                       +l+
     4325626CD1    98    AYKGMPMNIRGPMWSVLLNTEEM--------------------KLK 123


                   dkdeYeellnknkektvqdqneKssvgirrldyVEAVEKHPLSDDNDKTK
                   ++++Y+    +k+k + +
     4325626CD1   124 NPGRYQIMKEKGKRSSEH------------------------------- 141


                   GSLekgsdekalklredldkIekDlsRTfpdeiffqtrlaeqqlkkdqdl
                                   +++I++D+s T+++ iff+ r
     4325626CD1   142 ----------------IQRIDRDVSGTLRKHIFFRDR------------ 162


                   daydkDEfddeddkneppsikqLrrlLvaYswknpqehlgYvQGMnvils
                                  + ++ L +L aY +np    +gY+   + i++
     4325626CD1   163 ---------------YGTKQRELLHILLAYEEYNPE--VGYCRDLSHIAA 195


                   pLLlflkhgvdldeideeqAFwclvkLm..dnylpqkyflndlsglnedl
                   ++Ll l            +ee+AFw+lv L+ +++  +q +++++  +++  +
     4325626CD1   196 LFLLYL---------PEEDAFWALVQLLasERHSLQGFHSPNGGTVQGLQ 236


                   rvLdslvkeslPeLyshlkkkenktgsgkKknllaldltllifafpwfLt
                   + ++ v  s P+   h  kk            +    ++ +  ++++
     4325626CD1   237 DQQEHVVATSQPKTMGHQDKK--------------DLCGQCSPLGCLIRI 272


                   lFarelPleivlrIwDilftyYlgshflifvalAiLkllkskllkh<-*
                   l ++  +l  +lr+wD+++ +  g + l  +     +k  +  l k
     4325626CD1   273 L-IDGISLGLTLRLWDVYLVE--GEQALMPITRIAFKVQQKRLTKT      315


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